



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,445B
Source: IFW16
Date Processed by STIC: 10-12-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!) (ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number: <400> sequence id number: 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See, "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

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4 <110> APPLICANT: BARCLAY, A. Neil
5      BROWN, Marion H.
6      GORMAN, Daniel M.
7      LANIER, Lewis L.
8      WRIGHT, Gavin J.
9      CHERWINSKI, Holly
10     PHILLIPS, Joseph H.
11     HOEK, Robert M.
12     SEDGWICK, Jonathan D.
14 <120> TITLE OF INVENTION: OX2 RECEPTOR HOMOLOGS (AS AMENDED)
16 <130> FILE REFERENCE: 140942000900
18 <140> CURRENT APPLICATION NUMBER: US 10/009,445B
19 <141> CURRENT FILING DATE: 2001-11-13
21 <150> PRIOR APPLICATION NUMBER: PCT US00/12998
22 <151> PRIOR FILING DATE: 2000-05-11
24 <150> PRIOR APPLICATION NUMBER: GB 9925989.7
25 <151> PRIOR FILING DATE: 1999-11-03
28 <150> PRIOR APPLICATION NUMBER: GB 9911123.9
29 <151> PRIOR FILING DATE: 1999-05-13
31 <160> NUMBER OF SEQ ID NOS: 70
33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1574
38 <212> TYPE: DNA
39 <213> ORGANISM: Unknown
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42 <223> OTHER INFORMATION: Description of Unknown Organism: rodent; surmised
43      rattus rattus
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46 <221> NAME/KEY: CDS
47 <222> LOCATION: (91)..(1071)
49 <220> FEATURE:
50 <221> NAME/KEY: mat_peptide
51 <222> LOCATION: (162)..(1071)
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57                      Met Leu Cys Phe Trp Arg Thr Ser
58                               -20
60 cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt 162
61 His Val Ala Val Leu Ile Trp Gly Val Phe Ala Ala Glu Ser Ser
62      -15          -10          -5          -1
64 tgt cct gat aag aat caa aca atg cag aac aat tca tca act atg aca 210

```

(pg.6-7)
 Does Not Comply
 Corrected Diskette Needed

(pg.3,6)

RAW SEQUENCE LISTING

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DATE: 10/12/2004

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

65	Cys Pro Asp Lys Asn Gln Thr Met Gln Asn Asn Ser Ser Thr Met Thr	
66	1 5 10 15	
68	gaa gtt aac act aca gtg ttt gta cag atg ggt aaa aag gct ctg ctc	258
69	Glu Val Asn Thr Thr Val Phe Val Gln Met Gly Lys Lys Ala Leu Leu	
70	20 25 30	
72	tgc tgc cct tct att tca ctg aca aaa gta ata tta ata aca tgg aca	306
73	Cys Cys Pro Ser Ile Ser Leu Thr Lys Val Ile Leu Ile Thr Trp Thr	
74	35 40 45	
76	ata acc ctc aga gga cag cct tcc tgc ata ata tcc tac aaa gca gac	354
77	Ile Thr Leu Arg Gly Gln Pro Ser Cys Ile Ile Ser Tyr Lys Ala Asp	
78	50 55 60	
80	aca agg gag acc cat gaa agc aac tgc tcg gac aga agc atc acc tgg	402
81	Thr Arg Glu Thr His Glu Ser Asn Cys Ser Asp Arg Ser Ile Thr Trp	
82	65 70 75 80	
84	gcc tcc aca cct gac ctc gct cct gac ctt cag atc agt gca gtg gcc	450
85	Ala Ser Thr Pro Asp Leu Ala Pro Asp Leu Gln Ile Ser Ala Val Ala	
86	85 90 95	
88	ctc cag cat gaa ggg cgt tac tca tgt gat ata gca gta cct gac ggg	498
89	Leu Gln His Glu Gly Arg Tyr Ser Cys Asp Ile Ala Val Pro Asp Gly	
90	100 105 110	
92	aat ttc caa aac atc tat gac ctc caa gtg ctg gtg ccc cct gaa gta	546
93	Asn Phe Gln Asn Ile Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val	
94	115 120 125	
96	acc cac ttt cca ggg gaa aat aga act gca gtt tgt gag gcg att gca	594
97	Thr His Phe Pro Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Ile Ala	
98	130 135 140	
100	ggc aaa cct gct gcg cag atc tct tgg acg cca gat ggg gat tgt gtc	642
101	Gly Lys Pro Ala Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val	
102	145 150 155 160	
104	gct aag aat gaa tca cac agc aat ggc acc gtg act gtc cgg agc aca	690
105	Ala Lys Asn Glu Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr	
106	165 170 175	
108	tgc cac tgg gag cag agc cac gtg tct gtc gtg ttc tgt gtt gtc tct	738
109	Cys His Trp Glu Gln Ser His Val Ser Val Val Phe Cys Val Val Ser	
110	180 185 190	
112	cac ttg aca act ggt aac cag tct ctg tct ata gaa ctg ggt aga ggg	786
113	His Leu Thr Thr Gly Asn Gln Ser Leu Ser Ile Glu Leu Gly Arg Gly	
114	195 200 205	
116	ggt gac caa tta tta gga tca tac att caa tac atc atc cca tct att	834
117	Gly Asp Gln Leu Leu Gly Ser Tyr Ile Gln Tyr Ile Ile Pro Ser Ile	
118	210 215 220	
120	att att ttg atc atc ata gga tgc att tgt ctt ttg aaa atc agt ggc	882
121	Ile Ile Leu Ile Ile Gly Cys Ile Cys Leu Leu Lys Ile Ser Gly	
122	225 230 235 240	
124	tgc aga aaa tgt aaa ttg cca aaa tcg gga gct act cca gat att gag	930
125	Cys Arg Lys Cys Lys Leu Pro Lys Ser Gly Ala Thr Pro Asp Ile Glu	
126	245 250 255	
128	gag gat gaa atg cag ccg tat gct agc tac aca gag aag agc aat cca	978
129	Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Ser Asn Pro	

RAW SEQUENCE LISTING

DATE: 10/12/2004

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TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seglist.txt

Output Set: N:\CRP4\10122004\J009445B.raw

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132 ctc tat gat act gtg acc acg acg gag gca cac cca gcg tca caa ggc			1026
133 Leu Tyr Asp Thr Val Thr Thr Glu Ala His Pro Ala Ser Gln Gly			
134 275	280	285	
136 aaa gtc aat ggc aca gac tgt ctt act ttg tca gcc atg gga atc			1071
137 Lys Val Asn Gly Thr Asp Cys Leu Thr Leu Ser Ala Met Gly Ile			
138 290	295	300	
140 tagaaccaag gaaaagaagt caagagacat cataattact gctttcttt cttaaactt			1131
142 ctccaatggg gggaaattag ctcttctgaa gttcttagaa agcacaatg ttctaatgg			1191
144 ttgccttta agttttcta tcatttggaaat tttggatct ttgtctgtac ctgttaattt			1251
146 taggaagaac tgatattttt attacaaaga aagcacattt ttatgttaaa atatcaaatt			1311
148 gtgcaatacata atgatgaaaa ctgagttcc tcaagaaata actgcagaag gaacaatcat			1371
150 tactaaagca ttcatgtga gttcttccaa aaaagaaaaat ccctgtgtat acgacatgt			1431
152 tatggatgt gtgtgcctt atatgttgt ttacaaatgt gtatatatgc acacatctga			1491
154 ttatcaagac atctctgtca aaaactcaact ggcttccag atttatgaaa gctaataaag			1551
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160 <211> LENGTH: 327			
161 <212> TYPE: PRT			
162 <213> ORGANISM: Unknown			
164 <220> FEATURE:			
164 <223> OTHER INFORMATION:			
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168 Gly Val Phe Ala Ala Glu Ser Ser Cys Pro Asp Lys Asn Gln Thr Met			
169 -5 -1 1 5			
171 Gln Asn Asn Ser Ser Thr Met Thr Glu Val Asn Thr Thr Val Phe Val			
172 10 15 20			
174 Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr			
175 25 30 35 40			
177 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser			
178 45 50 55			
180 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn			The type of
181 60 65 70			the Sequence
183 Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro			Sequence
184 75 80 85			
187 Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser			
188 90 95 100			
190 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu			
191 105 110 115 120			
193 Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg			
194 125 130 135			
196 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser			
197 140 145 150			
199 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn			
200 155 160 165			
202 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val			
203 170 175 180			

• Pls see error explanation on pg 8. ↓
- Pls insert, whenever <213> response
is artificial
Unknown or
Genus/Species.

<213> response
is artificial
Unknown or
genus/species.

AS1 The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004
TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

205 Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
206 185 190 195 200
208 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
209 205 210 215
211 Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Ile Ile Gly Cys
212 220 225 230
214 Ile Cys Leu Leu Lys Ile Ser Gly Cys Arg Lys Cys Lys Leu Pro Lys
215 235 240 245
217 Ser Gly Ala Thr Pro Asp Ile Glu Asp Glu Met Gln Pro Tyr Ala
218 250 255 260
220 Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Thr Thr
221 265 270 275 280
223 Glu Ala His Pro Ala Ser Gln Gly Lys Val Asn Gly Thr Asp Cys Leu
224 285 290 295
226 Thr Leu Ser Ala Met Gly Ile
227 300
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231 <211> LENGTH: 1604
232 <212> TYPE: DNA
233 <213> ORGANISM: Unknown
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Unknown Organism: primate; surmised
237 homo sapiens
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241 <222> LOCATION: (217)..(1101)
243 <220> FEATURE:
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245 <222> LOCATION: (295)..(1101)
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252 aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa 180
254 agtacttgat gaaggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga 234
255 Met Leu Cys Pro Trp Arg
256 -25
258 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc 282
259 Thr Ala Asn Leu Gly Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
260 -20 -15 -10 -5
262 gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act 330
263 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
264 -1 1 5 10
266 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa 378
267 Ser Lys Glu Asn His Ala Leu Ala Ser Ser Leu Cys Met Asp Glu
268 15 20 25
270 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act 426
271 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
272 30 35 40
274 tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct 474

RAW SEQUENCE LISTING DATE: 10/12/2004
 PATENT APPLICATION: US/10/009,445B TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

275 Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro		
276 45 50 55 60		
278 atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga	522	
279 Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg		
280 65 70 75		
282 ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc	570	
283 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr		
284 80 85 90		
286 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct	618	
287 Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro		
288 95 100 105		
290 gat cag aat tcg gac ctt cag att cgt acc gtg gcc atc act cat gac	666	
291 Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr Val Ala Ile Thr His Asp		
292 110 115 120		
294 ggg tat tac aga tgc ata atg gta aca cct gat ggg aat ttc cat cgt	714	
295 Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg		
296 125 130 135 140		
298 gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa	762	
299 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln		
300 145 150 155		
302 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct	810	
303 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala		
304 160 165 170		
306 gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa	858	
307 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu		
308 175 180 185		
310 tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag	906	
311 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu		
312 190 195 200		
314 gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc	954	
315 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly		
316 205 210 215 220		
318 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa	1002	
319 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys		
320 225 230 235		
322 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta	1050	
323 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Leu		
324 240 245 250		
326 gac cat cgt ggg att cat ttg gtt gaa agt caa tgg ctg cag aaa	1098	
327 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys		
328 255 260 265		
330 ata taaaattgaat aaaacagaat ctactccagt tggtgaggag gatgaaatgc	1151	
331 Ile		
333 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaaggta	1211	
335 aggcatctga ggcattacaa agtgaagttg acacagacct ccatacttta taagtttttg	1271	
337 gactcttagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct	1331	
339 tacagttcta gaatgaagac ttatattgaa attagtttt ccaaggttct tagaagacat	1391	
341 ttaatggat tctcattcat acccttgtat aattggaaatt ttgattttt agctgctacc	1451	
343 agcttagttct ctgaagaact gatgttatta caaagaaaat acatgccccat gaccaaatat	1511	

<210> 21

<211> 1044

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(1044)

<223> n may be a, c, g, or t

<400> 21

INVALID
Response

Mandatory, <213>

Responses has to be
either artificial/
Unknown or Genus/
Species. Pls see
item #10 on
error summary
Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:14; N Pos. 552,558,561,564,567,576,579,582,585,591,594,597,606,615,621
Seq#:14; N Pos. 630,633,651,657,660,663,666,669,675,678,693,702,705,708,711
Seq#:14; N Pos. 714,723,726,732,735,738,747,750,762,765,768,771,774,777,780
Seq#:14; N Pos. 792,807,819,834,843,846,855,858,861,867,876
Seq#:15; N Pos. 18,21,24,27,30,33,36,39,42,51,54,60,63,66,69,72,78,93,96
Seq#:15; N Pos. 108,111,114,117,120,123,129,135,138,141,144,147,156,159,165
Seq#:15; N Pos. 168,171,183,189,192,195,201,204,207,213,228,231,234,237,240
Seq#:15; N Pos. 243,249,255,264,270,276,285,288,294,297,300,309,315,318,321
Seq#:15; N Pos. 324,333,336,342,351,354,357,360,363,375,378,384,393,396,399
Seq#:15; N Pos. 402,408,432,438,441,444,447,450,456,459,468,480,483,486,489
Seq#:15; N Pos. 498,504,507,513,516,519,528,534,537,543,552,555,558,561,567
Seq#:15; N Pos. 573,579,582,585,588,591,594,597,600,624,627,633,636,645,648
Seq#:15; N Pos. 654,657,660,669,672,675,684,687,690,693,696,705,708,711,714
Seq#:15; N Pos. 723,735,738,750,762,774,777,786,789,795,807,810,816,822,825
Seq#:15; N Pos. 828,831,855,861,864,870,879,885,888,897,900,903,909,915,921
Seq#:15; N Pos. 924,927,933,939,945,948,957,960,963,966,969,975
Seq#:16; N Pos. 6,9,21,33,36,45,51,60,66,69,72,87,90,93,102,105,111,114,117
Seq#:16; N Pos. 123,135,150,153,156,162,165,171,177,192,201,210,219,222,228
Seq#:16; N Pos. 234,240,243,246,249,261,267,276,279,282,288,291,300,309,312
Seq#:16; N Pos. 318,321,324,327,333,345,348,357,363,366,369,372,375,381,387
Seq#:16; N Pos. 396,399,408,411,414,423,426,429,432,438,441,444,453,462,468
Seq#:16; N Pos. 471,477,480,483,501,507,510,513,516,519,525,528,534,543,552
Seq#:16; N Pos. 555,558,561,570,573,579,582,585,594,597,600,603,609,615,618
Seq#:16; N Pos. 621,624,627,630,633,636,639,642,645,648,651,654,663,669,675
Seq#:16; N Pos. 678,681,687,690,696,699,702,705,708,714,726,738,741,747,750
Seq#:17; N Pos. 3,6,12,15,27,36,42,51,60,66,69,72,81,87,90,93,96,108,114

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Seq#:17; N Pos. 123,126,129,132,135,147,156,168,171,174,180,195,204,210,213
Seq#:17; N Pos. 216,219,222,228,231,240,243,252,255,258,261,270,276,279,285
Seq#:17; N Pos. 288,291,300,306,309,315,324,327,333,339,345,351,354,357,360
Seq#:17; N Pos. 363,366,369,372,396,399,402,405,408,417,420,426,429,432,441
Seq#:17; N Pos. 444,447,456,459,462,465,468,471,474,477,480,483,486,489,492
Seq#:17; N Pos. 495,501,507,516,519,522,525,534,537,543,546,552,567,573,576
Seq#:17; N Pos. 579,582

Use of <220> Feature(NEW RULES): Error Explanation:
Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2,4,6,8,10,12,20,23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004

TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

L:164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>

ORGANISM:Unknown

L:164 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>

ORGANISM:Unknown

L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2, Line#:164

L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>

ORGANISM:Unknown

L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>

ORGANISM:Unknown

L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4, Line#:355

L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>

ORGANISM:Unknown

L:541 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>

ORGANISM:Unknown

L:541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6, Line#:541

L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>

ORGANISM:Unknown

L:699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>

ORGANISM:Unknown

L:699 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8, Line#:699

L:836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>

ORGANISM:Unknown

L:836 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>

ORGANISM:Unknown

L:836 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10, Line#:836

L:992 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>

ORGANISM:Unknown

L:992 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>

ORGANISM:Unknown

L:992 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12, Line#:992

L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

M:341 Repeated in SeqNo=13

L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

M:341 Repeated in SeqNo=14

L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

M:341 Repeated in SeqNo=15

L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0

M:341 Repeated in SeqNo=16

L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

M:341 Repeated in SeqNo=17

L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0

M:341 Repeated in SeqNo=18

L:1405 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>

ORGANISM:Unknown

L:1405 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>

ORGANISM:Unknown

L:1405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20, Line#:1405

L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

M:341 Repeated in SeqNo=21

L:1614 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>

ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>

ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1614
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24